

SEQUENCE LISTING

<110> C. Frank Bennett
Kenneth W. Dobie
Susan Gregory

<120> MODULATION OF DC-SIGN EXPRESSION

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ctg gag gag gaa cag ctg aga ggc ctt gga ttc cga cag act cga gga 99

Leu Glu Glu Glu Gln Leu Arg Gly Leu Gly Phe Arg Gln Thr Arg Gly

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tac aag agc tta gca ggg tgt ctt ggc cat ggt ccc ctg gtg ctg caa 147

Tyr Lys Ser Leu Ala Gly Cys Leu Gly His Gly Pro Leu Val Leu Gln

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ctc ctc tcc ttc acg ctc ttg gct ggg ctc ctt gtc caa gtg tcc aag 195

Leu Leu Ser Phe Thr Leu Leu Ala Gly Leu Leu Val Gln Val Ser Lys

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gtc ccc agc tcc ata agt cag gaa caa tcc agg caa gac gcg atc tac 243
 Val Pro Ser Ser Ile Ser Gln Glu Gln Ser Arg Gln Asp Ala Ile Tyr
 65 70 75

cag aac ctg acc cag ctt aaa gct gca gtg ggt gag ctc tca gag aaa 291
 Gln Asn Leu Thr Gln Leu Lys Ala Ala Val Gly Glu Leu Ser Glu Lys
 80 85 90

tcc aag ctg cag gag atc tac cag gag ctg acc cag ctg aag gct gca 339
 Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Gln Leu Lys Ala Ala
 95 100 105 110

gtg ggt gag ctt cca gag aaa tct aag ctg cag gag atc tac cag gag 387
 Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu
 115 120 125

ctg acc cgg ctg aag gct gca gtg ggt gag ctt cca gag aaa tct aag 435
 Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys
 130 135 140

ctg cag gag atc tac cag gag ctg acc tgg ctg aag gct gca gtg ggt 483
 Leu Gln Glu Ile Tyr Gln Glu Leu Thr Trp Leu Lys Ala Ala Val Gly
 145 150 155

gag ctt cca gag aaa tct aag atg cag gag atc tac cag gag ctg act 531
 Glu Leu Pro Glu Lys Ser Lys Met Gln Glu Ile Tyr Gln Glu Leu Thr
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 Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Gln Gln
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gag atc tac cag gag ctg acc cgg ctg aag gct gca gtg ggt gag ctt 627
 Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu
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cca gag aaa tct aag cag cag gag atc tac cag gag ctg acc cgg ctg 675
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Val Gly Ala Gln Leu Val Val Ile Lys Ser Ala Glu Glu Gln Asn Phe	
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Val Gly Glu Glu Asp Cys Ala Glu Phe Ser Gly Asn Gly Trp Asn Asp	
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370

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395

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111

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Leu	Arg	Pro	Leu	Asp	Glu	Glu	Leu	Leu	Thr	Ser	Ser	His	Thr	Arg	His	
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Tyr	Lys	Ile	Pro	Ser	Ser	Gln	Glu	Glu	Asn	Asn	Gln	Met	Asn	Val	Tyr	
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caa	gaa	ctg	acc	cag	ttg	aag	gct	ggc	gta	gat	cga	ctg	tgc	cgc	tcc	399
Gln	Glu	Leu	Thr	Gln	Leu	Lys	Ala	Gly	Val	Asp	Arg	Leu	Cys	Arg	Ser	
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Cys	Pro	Trp	Asp	Trp	Thr	His	Phe	Gln	Gly	Ser	Cys	Tyr	Phe	Phe	Ser	
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Val	Ala	Gln	Lys	Ser	Trp	Asn	Asp	Ser	Ala	Thr	Ala	Cys	His	Asn	Val	
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ggg	gct	caa	ctt	gtg	gtc	atc	aag	agt	gat	gaa	gag	cag	aac	ttt	cta	543
Gly	Ala	Gln	Leu	Val	Val	Ile	Lys	Ser	Asp	Glu	Glu	Gln	Asn	Phe	Leu	
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Met Ser Lys Glu Ser Thr Trp Tyr Trp Val Asp Gly Ser Pro Leu Thr	
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ctc agt ttc atg aag tat tgg agt aaa gga gaa cct aac aac ctg gga	687
Leu Ser Phe Met Lys Tyr Trp Ser Lys Gly Glu Pro Asn Asn Leu Gly	
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tgt act aac aag aaa ttc tgg atc tgc aaa aag ctt tca act tcc tgc	783
Cys Thr Asn Lys Lys Phe Trp Ile Cys Lys Lys Leu Ser Thr Ser Cys	
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<400> 13

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<211> 23

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catccagcca caccaggcac tcc

23

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<213> H. sapiens

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5

10

15

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agc tta gca ggg tgt ctt ggc cat ggt ccc ctg gtg ctg caa ctc ctc	144
Ser Leu Ala Gly Cys Leu Gly His Gly Pro Leu Val Leu Gln Leu Leu	
35 40 45	
tcc ttc acg ctc ttg gct ggg ctc ctt gtc caa gtg tcc aag gtc ccc	192
Ser Phe Thr Leu Leu Ala Gly Leu Leu Val Gln Val Ser Lys Val Pro	
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Ser Ser Ile Ser Gln Glu Gln Ser Arg Gln Asp Ala Ile Tyr Gln Asn	
65 70 75 80	
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Leu Thr Gln Leu Lys Ala Ala Val Gly Glu Leu Ser Glu Lys Ser Lys	
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Leu Gln Glu Ile Tyr Gln Glu Leu Thr Gln Leu Lys Ala Ala Val Gly	
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cgg ctg aag gct gca gtg ggt gag ctt cca gag aaa tct aag ctg cag	432
Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln	
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Glu Ile Tyr Gln Glu Leu Thr Trp Leu Lys Ala Ala Val Gly Glu Leu	
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165 170 175	

aag gct gca gtg ggt gag ctt cca gag aaa tct aag cag cag gag atc	576
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Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu	
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Lys Ser Lys Gln Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala	
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Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Gln Gln Glu Ile Tyr Gln	
225 230 235 240	
gag ctg acc cag ctg aag gct gca gtg gaa cgc ctg tgc cac ccc tgt	768
Glu Leu Thr Gln Leu Lys Ala Ala Val Glu Arg Leu Cys His Pro Cys	
245 250 255	
ccc tgg gaa tgg aca ttc ttc caa gga aac tgt tac ttc atg tct aac	816
Pro Trp Glu Trp Thr Phe Phe Gln Gly Asn Cys Tyr Phe Met Ser Asn	
260 265 270	
tcc cag cgg aac tgg cac gac tcc atc acc gcc tgc aaa gaa gtg ggg	864
Ser Gln Arg Asn Trp His Asp Ser Ile Thr Ala Cys Lys Glu Val Gly	
275 280 285	
gcc cag ctc gtc gta atc aaa agt gct gag gag cag tct tcc aga agt	912
Ala Gln Leu Val Val Ile Lys Ser Ala Glu Glu Gln Ser Ser Arg Ser	
290 295 300	
aac cgc ttc acc tgg atg gga ctt tca gat cta aat cag gaa ggc acg	960
Asn Arg Phe Thr Trp Met Gly Leu Ser Asp Leu Asn Gln Glu Gly Thr	
305 310 315 320	
tgg caa tgg gtg gac ggc tca cct ctg ttg ccc agc ttc aag cag tat	1008
Trp Gln Trp Val Asp Gly Ser Pro Leu Leu Pro Ser Phe Lys Gln Tyr	

325	330	335	
tgg aac aga gga gag ccc aac aac gtt ggg gag gaa gac tgc gcg gaa			1056
Trp Asn Arg Gly Glu Pro Asn Asn Val Gly Glu Glu Asp Cys Ala Glu			
340	345	350	
ttt agt ggc aat ggc tgg aac gac gac aaa tgt aat ctt gcc aaa ttc			1104
Phe Ser Gly Asn Gly Trp Asn Asp Asp Lys Cys Asn Leu Ala Lys Phe			
355	360	365	
tgg atc tgc aaa aag tcc gca gcc tcc tgc tcc agg gat gaa gaa cag			1152
Trp Ile Cys Lys Lys Ser Ala Ala Ser Cys Ser Arg Asp Glu Glu Gln			
370	375	380	
ttt ctt tct cca gcc cct gcc acc cca aac ccc cct cct gcg tag			1197
Phe Leu Ser Pro Ala Pro Ala Thr Pro Asn Pro Pro Pro Ala			
385	390	395	

1197

<210> 20

<211> 939

<212> DNA

<213> H. sapiens

<220>

<220>

<221> CDS

<222> (1) ... (939)

<400> 20

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Met Ser Asp Ser Lys Glu Pro Arg Leu Gln Gln Leu Gly Leu Leu Glu	
1 5 10 15	

gag gaa cag ctg aga ggc ctt gga ttc cga cag act cga gga tac aag	96
Glu Glu Gln Leu Arg Gly Leu Gly Phe Arg Gln Thr Arg Gly Tyr Lys	

	20	25	30	
agc tta gca ggg tgt ctt ggc cat ggt ccc ctg gtg ctg caa ctc ctc				144
Ser Leu Ala Gly Cys Leu Gly His Gly Pro Leu Val Leu Gln Leu Leu				
	35	40	45	
tcc ttc acg ctc ttg gct ggg ctc ctt gtc caa gtg tcc aag gtc ccc				192
Ser Phe Thr Leu Leu Ala Gly Leu Leu Val Gln Val Ser Lys Val Pro				
	50	55	60	
agc tcc ata agt cag gaa caa tcc agg caa gac gcg atc tac cag aac				240
Ser Ser Ile Ser Gln Glu Gln Ser Arg Gln Asp Ala Ile Tyr Gln Asn				
	65	70	75	80
ctg acc cag ctt aaa gct gca gtg ggt gag ctc tca gag aaa tcc aag				288
Leu Thr Gln Leu Lys Ala Ala Val Gly Glu Leu Ser Glu Lys Ser Lys				
	85	90	95	
ctg cag gag atc tac cag gag ctg acc cag ctg aag gct gca gtg ggt				336
Leu Gln Glu Ile Tyr Gln Glu Leu Thr Gln Leu Lys Ala Ala Val Gly				
	100	105	110	
gag ctt cca gag aaa tct aag ctg cag gag atc tac cag gag ctg acc				384
Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr				
	115	120	125	
cgg ctg aag gct gca gtg ggt gag ctt cca gag aaa tct aag ctg cag				432
Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln				
	130	135	140	
gag atc tac cag gag ctg acc cag ctg aag gct gca gtg gaa cgc ctg				480
Glu Ile Tyr Gln Glu Leu Thr Gln Leu Lys Ala Ala Val Glu Arg Leu				
	145	150	155	160
tgc cac ccc tgt ccc tgg gaa tgg aca ttc ttc caa gga aac tgt tac				528
Cys His Pro Cys Pro Trp Glu Trp Thr Phe Phe Gln Gly Asn Cys Tyr				
	165	170	175	
ttc atg tct aac tcc cag cgg aac tgg cac gac tcc atc acc gcc tgc				576

Phe Met Ser Asn Ser Gln Arg Asn Trp His Asp Ser Ile Thr Ala Cys
 180 185 190

aaa gaa gtg ggg gcc cag ctc gtc gta atc aaa agt gct gag gag cag 624
 Lys Glu Val Gly Ala Gln Leu Val Val Ile Lys Ser Ala Glu Glu Gln
 195 200 205

aac ttc cta cag ctg cag tct tcc aga agt aac cgc ttc acc tgg atg 672
 Asn Phe Leu Gln Leu Gln Ser Ser Arg Ser Asn Arg Phe Thr Trp Met
 210 215 220

gga ctt tca gat cta aat cag gaa ggc acg tgg caa tgg gtg gac ggc 720
 Gly Leu Ser Asp Leu Asn Gln Glu Gly Thr Trp Gln Trp Val Asp Gly
 225 230 235 240

tca cct ctg ttg ccc agc ttc aag cag tat tgg aac aga gga gag ccc 768
 Ser Pro Leu Leu Pro Ser Phe Lys Gln Tyr Trp Asn Arg Gly Glu Pro
 245 250 255

aac aac gtt ggg gag gaa gac tgc gcg gaa ttt agt ggc aat ggc tgg 816
 Asn Asn Val Gly Glu Glu Asp Cys Ala Glu Phe Ser Gly Asn Gly Trp
 260 265 270

aac gac gac aaa tgt aat ctt gcc aaa ttc tgg atc tgc aaa aag tcc 864
 Asn Asp Asp Lys Cys Asn Leu Ala Lys Phe Trp Ile Cys Lys Lys Ser
 275 280 285

gca gcc tcc tgc tcc agg gat gaa gaa cag ttt ctt tct cca gcc cct 912
 Ala Ala Ser Cys Ser Arg Asp Glu Glu Gln Phe Leu Ser Pro Ala Pro
 290 295 300

gcc acc cca aac ccc cct cct gcg tag 939
 Ala Thr Pro Asn Pro Pro Pro Ala
 305 310

<210> 21

<211> 507

<212> DNA

<213> H. sapiens

<220>

<220>

<221> CDS

<222> (1)...(507)

<400> 21

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Met Ser Asp Ser Lys Glu Pro Arg Leu Gln Gln Leu Gly Leu Leu Glu	
1 5 10 15	
 gag gaa cag ctg aga ggc ctt gga ttc cga cag act cga gga tac aag	96
Glu Glu Gln Leu Arg Gly Leu Gly Phe Arg Gln Thr Arg Gly Tyr Lys	
20 25 30	
 agc tta gca ggg tgt ctt ggc cat ggt ccc ctg gtg ctg caa ctc ctc	144
Ser Leu Ala Gly Cys Leu Gly His Gly Pro Leu Val Leu Gln Leu Leu	
35 40 45	
 tcc ttc acg ctc ttg gct ggg ctc ctt gtc caa gtg tcc aag gtc ccc	192
Ser Phe Thr Leu Leu Ala Gly Leu Leu Val Gln Val Ser Lys Val Pro	
50 55 60	
 agc tcc ata agt cag gaa caa tcc aga agt aac cgc ttc acc tgg atg	240
Ser Ser Ile Ser Gln Glu Gln Ser Arg Ser Asn Arg Phe Thr Trp Met	
65 70 75 80	
 gga ctt tca gat cta aat cag gaa ggc acg tgg caa tgg gtg gac ggc	288
Gly Leu Ser Asp Leu Asn Gln Glu Gly Thr Trp Gln Trp Val Asp Gly	
85 90 95	
 tca cct ctg ttg ccc agc ttc aag cag tat tgg aac aga gga gag ccc	336
Ser Pro Leu Leu Pro Ser Phe Lys Gln Tyr Trp Asn Arg Gly Glu Pro	
100 105 110	
 aac aac gtt ggg gag gaa gac tgc gcg gaa ttt agt ggc aat ggc tgg	384
Asn Asn Val Gly Glu Glu Asp Cys Ala Glu Phe Ser Gly Asn Gly Trp	

agg caa gac gcg atc tac cag aac ctg acc cag ctt aaa gct gca gtg	192
Arg Gln Asp Ala Ile Tyr Gln Asn Leu Thr Gln Leu Lys Ala Ala Val	
50 55 60	
ggt gag ctc tca gag aaa tcc aag ctg cag gag atc tac cag gag ctg	240
Gly Glu Leu Ser Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu	
65 70 75 80	
acc cag ctg aag gct gca gtg ggt gag ctt cca gag aaa tct aag ctg	288
Thr Gln Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu	
85 90 95	
cag gag atc tac cag gag ctg acc cgg ctg aag gct gca gtg ggt gag	336
Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu	
100 105 110	
ctt cca gag aaa tct aag ctg cag gag atc tac cag gag ctg acc tgg	384
Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Trp	
115 120 125	
ctg aag gct gca gtg ggt gag ctt cca gag aaa tct aag atg cag gag	432
Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Met Gln Glu	
130 135 140	
atc tac cag gag ctg act cgg ctg aag gct gca gtg ggt gag ctt cca	480
Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu Pro	
145 150 155 160	
gag aaa tct aag cag cag gag atc tac cag gag ctg acc cgg ctg aag	528
Glu Lys Ser Lys Gln Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys	
165 170 175	
gct gca gtg ggt gag ctt cca gag aaa tct aag cag cag gag atc tac	576
Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Gln Gln Glu Ile Tyr	
180 185 190	
cag gag ctg acc cgg ctg aag gct gca gtg ggt gag ctt cca gag aaa	624
Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys	
195 200 205	

tct aag cag cag gag atc tac cag gag ctg acc cag ctg aag gct gca	672
Ser Lys Gln Gln Glu Ile Tyr Gln Glu Leu Thr Gln Leu Lys Ala Ala	
210 215 220	
gtg gaa cgc ctg tgc cac ccc tgt ccc tgg gaa tgg aca ttc ttc caa	720
Val Glu Arg Leu Cys His Pro Cys Pro Trp Glu Trp Thr Phe Phe Gln	
225 230 235 240	
gga aac tgt tac ttc atg tct aac tcc cag cgg aac tgg cac gac tcc	768
Gly Asn Cys Tyr Phe Met Ser Asn Ser Gln Arg Asn Trp His Asp Ser	
245 250 255	
atc acc gcc tgc aaa gaa gtg ggg gcc cag ctc gtc gta atc aaa agt	816
Ile Thr Ala Cys Lys Glu Val Gly Ala Gln Leu Val Val Ile Lys Ser	
260 265 270	
gct gag gag cag aac ttc cta cag ctg cag tct tcc aga agt aac cgc	864
Ala Glu Glu Gln Asn Phe Leu Gln Leu Gln Ser Ser Arg Ser Asn Arg	
275 280 285	
ttc acc tgg atg gga ctt tca gat cta aat cag gaa ggc acg tgg caa	912
Phe Thr Trp Met Gly Leu Ser Asp Leu Asn Gln Glu Gly Thr Trp Gln	
290 295 300	
tgg gtg gac ggc tca cct ctg ttg ccc agc ttc aag cag tat tgg aac	960
Trp Val Asp Gly Ser Pro Leu Leu Pro Ser Phe Lys Gln Tyr Trp Asn	
305 310 315 320	
aga gga gag ccc aac aac gtt ggg gag gaa gac tgc gcg gaa ttt agt	1008
Arg Gly Glu Pro Asn Asn Val Gly Glu Glu Asp Cys Ala Glu Phe Ser	
325 330 335	
ggc aat ggc tgg aac gac gac aaa tgt aat ctt gcc aaa ttc tgg atc	1056
Gly Asn Gly Trp Asn Asp Asp Lys Cys Asn Leu Ala Lys Phe Trp Ile	
340 345 350	
tgc aaa aag tcc gca gcc tcc tgc tcc agg gat gaa gaa cag ttt ctt	1104
Cys Lys Lys Ser Ala Ala Ser Cys Ser Arg Asp Glu Glu Gln Phe Leu	

355

360

365

tct cca gcc cct gcc acc cca aac ccc cct cct gcg tag

1143

Ser Pro Ala Pro Ala Thr Pro Asn Pro Pro Pro Ala

370

375

380

<210> 23

<211> 1083

<212> DNA

<213> H. sapiens

<220>

<220>

<221> CDS

<222> (1)...(1083)

<400> 23

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48

Met Ser Asp Ser Lys Glu Pro Arg Leu Gln Gln Leu Gly Leu Leu Val

1

5

10

15

tcc aag gtc ccc agc tcc ata agt cag gaa caa tcc agg caa gac gcg

96

Ser Lys Val Pro Ser Ser Ile Ser Gln Glu Gln Ser Arg Gln Asp Ala

20

25

30

atc tac cag aac ctg acc cag ctt aaa gct gca gtg ggt gag ctc tca

144

Ile Tyr Gln Asn Leu Thr Gln Leu Lys Ala Ala Val Gly Glu Leu Ser

35

40

45

gag aaa tcc aag ctg cag gag atc tac cag gag ctg acc cag ctg aag

192

Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Gln Leu Lys

50

55

60

gct gca gtg ggt gag ctt cca gag aaa tct aag ctg cag gag atc tac

240

Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr

65

70

75

80

cag gag ctg acc cgg ctg aag gct gca gtg ggt gag ctt cca gag aaa	288
Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys	
85 90 95	
tct aag ctg cag gag atc tac cag gag ctg acc tgg ctg aag gct gca	336
Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Trp Leu Lys Ala Ala	
100 105 110	
gtg ggt gag ctt cca gag aaa tct aag atg cag gag atc tac cag gag	384
Val Gly Glu Leu Pro Glu Lys Ser Lys Met Gln Glu Ile Tyr Gln Glu	
115 120 125	
ctg act cgg ctg aag gct gca gtg ggt gag ctt cca gag aaa tct aag	432
Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys	
130 135 140	
cag cag gag atc tac cag gag ctg acc cgg ctg aag gct gca gtg ggt	480
Gln Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly	
145 150 155 160	
gag ctt cca gag aaa tct aag cag cag gag atc tac cag gag ctg acc	528
Glu Leu Pro Glu Lys Ser Lys Gln Gln Glu Ile Tyr Gln Glu Leu Thr	
165 170 175	
cgg ctg aag gct gca gtg ggt gag ctt cca gag aaa tct aag cag cag	576
Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Gln Gln	
180 185 190	
gag atc tac cag gag ctg acc cag ctg aag gct gca gtg gaa cgc ctg	624
Glu Ile Tyr Gln Glu Leu Thr Gln Leu Lys Ala Ala Val Glu Arg Leu	
195 200 205	
tgc cac ccc tgt ccc tgg gaa tgg aca ttc ttc caa gga aac tgt tac	672
Cys His Pro Cys Pro Trp Glu Trp Thr Phe Phe Gln Gly Asn Cys Tyr	
210 215 220	
ttc atg tct aac tcc cag cgg aac tgg cac gac tcc atc acc gcc tgc	720
Phe Met Ser Asn Ser Gln Arg Asn Trp His Asp Ser Ile Thr Ala Cys	
225 230 235 240	

aaa gaa gtg ggg gcc cag ctc gtc gta atc aaa agt gct gag gag cag 768
Lys Glu Val Gly Ala Gln Leu Val Val Ile Lys Ser Ala Glu Glu Gln
245 250 255

aac ttc cta cag ctg cag tct tcc aga agt aac cgc ttc acc tgg atg 816
Asn Phe Leu Gln Leu Gln Ser Ser Arg Ser Asn Arg Phe Thr Trp Met
260 265 270

gga ctt tca gat cta aat cag gaa ggc acg tgg caa tgg gtg gac ggc 864
Gly Leu Ser Asp Leu Asn Gln Glu Gly Thr Trp Gln Trp Val Asp Gly
275 280 285

tca cct ctg ttg ccc agc ttc aag cag tat tgg aac aga gga gag ccc 912
Ser Pro Leu Leu Pro Ser Phe Lys Gln Tyr Trp Asn Arg Gly Glu Pro
290 295 300

aac aac gtt ggg gag gaa gac tgc gcg gaa ttt agt ggc aat ggc tgg 960
Asn Asn Val Gly Glu Glu Asp Cys Ala Glu Phe Ser Gly Asn Gly Trp
305 310 315 320

aac gac gac aaa tgt aat ctt gcc aaa ttc tgg atc tgc aaa aag tcc 1008
Asn Asp Asp Lys Cys Asn Leu Ala Lys Phe Trp Ile Cys Lys Lys Ser
325 330 335

gca gcc tcc tgc tcc agg gat gaa gaa cag ttt ctt tct cca gcc cct 1056
Ala Ala Ser Cys Ser Arg Asp Glu Glu Gln Phe Leu Ser Pro Ala Pro
340 345 350

gcc acc cca aac ccc cct cct gcg tag 1083
Ala Thr Pro Asn Pro Pro Pro Ala
355 360

<210> 24

<211> 1315

<212> DNA

<213> H. sapiens

<220>

<220>

<221> CDS

<222> (101)...(1315)

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Met Ala Ser Ala Cys
1 5

cca ggc tct gat ttc acg tct atc cat tca gag gag gaa cag ctg aga 163
Pro Gly Ser Asp Phe Thr Ser Ile His Ser Glu Glu Glu Gln Leu Arg
10 15 20

ggc ctt gga ttc cga cag act cga gga tac aag agc tta gca ggg tgt 211
Gly Leu Gly Phe Arg Gln Thr Arg Gly Tyr Lys Ser Leu Ala Gly Cys
25 30 35

ctt ggc cat ggt ccc ctg gtg ctg caa ctc ctc tcc ttc acg ctc ttg 259
Leu Gly His Gly Pro Leu Val Leu Gln Leu Leu Ser Phe Thr Leu Leu
40 45 50

gct ggg ctc ctt gtc caa gtg tcc aag gtc ccc agc tcc ata agt cag 307
Ala Gly Leu Leu Val Gln Val Ser Lys Val Pro Ser Ser Ile Ser Gln
55 60 65

gaa caa tcc agg caa gac gcg atc tac cag aac ctg acc cag ctt aaa 355
Glu Gln Ser Arg Gln Asp Ala Ile Tyr Gln Asn Leu Thr Gln Leu Lys
70 75 80 85

gct gca gtg ggt gag ctc tca gag aaa tcc aag ctg cag gag atc tac 403
Ala Ala Val Gly Glu Leu Ser Glu Lys Ser Lys Leu Gln Glu Ile Tyr
90 95 100

cag gag ctg acc cag ctg aag gct gca gtg ggt gag ctt cca gag aaa 451
Gln Glu Leu Thr Gln Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys

105	110	115	
tct aag ctg cag gag atc tac cag gag ctg acc cgg ctg aag gct gca			499
Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala			
120	125	130	
gtg ggt gag ctt cca gag aaa tct aag ctg cag gag atc tac cag gag			547
Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu			
135	140	145	
ctg acc tgg ctg aag gct gca gtg ggt gag ctt cca gag aaa tct aag			595
Leu Thr Trp Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys			
150	155	160	165
atg cag gag atc tac cag gag ctg act cgg ctg aag gct gca gtg ggt			643
Met Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly			
170	175	180	
gag ctt cca gag aaa tct aag cag cag gag atc tac cag gag ctg acc			691
Glu Leu Pro Glu Lys Ser Lys Gln Gln Glu Ile Tyr Gln Glu Leu Thr			
185	190	195	
cgg ctg aag gct gca gtg ggt gag ctt cca gag aaa tct aag cag cag			739
Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Gln Gln			
200	205	210	
gag atc tac cag gag ctg acc cgg ctg aag gct gca gtg ggt gag ctt			787
Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu			
215	220	225	
cca gag aaa tct aag cag cag gag atc tac cag gag ctg acc cag ctg			835
Pro Glu Lys Ser Lys Gln Gln Glu Ile Tyr Gln Glu Leu Thr Gln Leu			
230	235	240	245
aag gct gca gtg gaa cgc ctg tgc cac ccc tgt ccc tgg gaa tgg aca			883
Lys Ala Ala Val Glu Arg Leu Cys His Pro Cys Pro Trp Glu Trp Thr			
250	255	260	
ttc ttc caa gga aac tgt tac ttc atg tct aac tcc cag cgg aac tgg			931

Phe Phe Gln Gly Asn Cys Tyr Phe Met Ser Asn Ser Gln Arg Asn Trp	
265 270 275	
cac gac tcc atc acc gcc tgc aaa gaa gtg ggg gcc cag ctc gtc gta	979
His Asp Ser Ile Thr Ala Cys Lys Glu Val Gly Ala Gln Leu Val Val	
280 285 290	
atc aaa agt gct gag gag cag aac ttc cta cag ctg cag tct tcc aga	1027
Ile Lys Ser Ala Glu Glu Gln Asn Phe Leu Gln Leu Gln Ser Ser Arg	
295 300 305	
agt aac cgc ttc acc tgg atg gga ctt tca gat cta aat cag gaa ggc	1075
Ser Asn Arg Phe Thr Trp Met Gly Leu Ser Asp Leu Asn Gln Glu Gly	
310 315 320 325	
acg tgg caa tgg gtg gac ggc tca cct ctg ttg ccc agc ttc aag cag	1123
Thr Trp Gln Trp Val Asp Gly Ser Pro Leu Leu Pro Ser Phe Lys Gln	
330 335 340	
tat tgg aac aga gga gag ccc aac aac gtt ggg gag gaa gac tgc gcg	1171
Tyr Trp Asn Arg Gly Glu Pro Asn Asn Val Gly Glu Glu Asp Cys Ala	
345 350 355	
gaa ttt agt ggc aat ggc tgg aac gac gac aaa tgt aat ctt gcc aaa	1219
Glu Phe Ser Gly Asn Gly Trp Asn Asp Asp Lys Cys Asn Leu Ala Lys	
360 365 370	
ttc tgg atc tgc aaa aag tcc gca gcc tcc tgc tcc agg gat gaa gaa	1267
Phe Trp Ile Cys Lys Lys Ser Ala Ala Ser Cys Ser Arg Asp Glu Glu	
375 380 385	
cag ttt ctt tct cca gcc cct gcc acc cca aac ccc cct cct gcg tag	1315
Gln Phe Leu Ser Pro Ala Pro Ala Thr Pro Asn Pro Pro Pro Ala	
390 395 400	

<210> 25

<211> 994

<212> DNA

<213> H. sapiens

<220>

<220>

<221> CDS

<222> (101)...(994)

<400> 25

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ggacgctggg attctgggaa gggggaaggg atggccagcc atg gcc tca gcc tgc 115

Met Ala Ser Ala Cys

1 5

cca gcc tct gat ttc acg tct atc cat tca gag gag gaa cag ctg aga 163

Pro Gly Ser Asp Phe Thr Ser Ile His Ser Glu Glu Glu Gln Leu Arg

10 15 20

ggc ctt gga ttc cga cag act cga gga tac aag agc tta gca gtg tcc 211

Gly Leu Gly Phe Arg Gln Thr Arg Gly Tyr Lys Ser Leu Ala Val Ser

25 30 35

aag gtc ccc agc tcc ata agt cag gaa caa tcc agg caa gac gcg atc 259

Lys Val Pro Ser Ser Ile Ser Gln Glu Gln Ser Arg Gln Asp Ala Ile

40 45 50

tac cag aac ctg acc cag ctt aaa gct gca gtg ggt gag ctc tca gag 307

Tyr Gln Asn Leu Thr Gln Leu Lys Ala Ala Val Gly Glu Leu Ser Glu

55 60 65

aaa tcc aag ctg cag gag atc tac cag gag ctg acc cag ctg aag gct 355

Lys Ser Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Gln Leu Lys Ala

70 75 80 85

gca gtg ggt gag ctt cca gag aaa tct aag ctg cag gag atc tac cag 403

Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Leu Gln Glu Ile Tyr Gln

90 95 100

gag ctg acc cgg ctg aag gct gca gtg ggt gag ctt cca gag aaa tct	451
Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser	
105 110 115	
aag ctg cag gag atc tac cag gag ctg acc tgg ctg aag gct gca gtg	499
Lys Leu Gln Glu Ile Tyr Gln Glu Leu Thr Trp Leu Lys Ala Ala Val	
120 125 130	
ggt gag ctt cca gag aaa tct aag atg cag gag atc tac cag gag ctg	547
Gly Glu Leu Pro Glu Lys Ser Lys Met Gln Glu Ile Tyr Gln Glu Leu	
135 140 145	
act cgg ctg aag gct gca gtg ggt gag ctt cca gag aaa tct aag cag	595
Thr Arg Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Gln	
150 155 160 165	
cag gag atc tac cag gag ctg acc cgg ctg aag gct gca gtg ggt gag	643
Gln Glu Ile Tyr Gln Glu Leu Thr Arg Leu Lys Ala Ala Val Gly Glu	
170 175 180	
ctt cca gag aaa tct aag cag cag gag atc tac cag gag ctg acc cgg	691
Leu Pro Glu Lys Ser Lys Gln Gln Glu Ile Tyr Gln Glu Leu Thr Arg	
185 190 195	
ctg aag gct gca gtg ggt gag ctt cca gag aaa tct aag cag cag gag	739
Leu Lys Ala Ala Val Gly Glu Leu Pro Glu Lys Ser Lys Gln Gln Glu	
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